

SEQUENCE LISTING

#4

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<120> A method for the identification of anesthetics <130> f17b12prov3-humanTREK

<140> 09/503,089 <141> 2000-02-11

<160> 5

<170> Microsoft Word 2000

<210> 1 <211> 1236 <212> DNA <213> Homo sapiens

<220> <221> CDS <222> (1)..(1236)

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aaa ccg agg ctc tcg ttt tcc acg aaa ccc aca gtg ctt gct tcc cgg $\,$ 96 Lys Pro Arg Leu Ser Phe Ser Thr Lys Pro Thr Val Leu Ala Ser Arg $\,$ 20 $\,$ 25 $\,$ 30

gtg gag agt gac acg acc att aat gtt atg aaa tgg aag acg gtc tcc $\,$ 144 Val Glu Ser Asp Thr Thr Ile Asn Val Met Lys Trp Lys Thr Val Ser $\,$ 35 $\,$ 40 $\,$ 45

acg ata ttc ctg gtg gtt gtc ctc tat ctg atc atc gga gcc acc gtg 192
Thr Ile Phe Leu Val Val Leu Tyr Leu Ile Ile Gly Ala Thr Val
50 55 60

ttc aaa gca ttg gag cag cct cat gag att tca cag agg acc acc att $$ 240 Phe Lys Ala Leu Glu Gln Pro His Glu Ile Ser Gln Arg Thr Thr Ile $$ 65 $$ 70 $$ 75 $$ 80

gtg atc cag aag caa aca ttc ata tcc caa cat tcc tgt gtc aat tcg 288 Val Ile Gln Lys Gln Thr Phe Ile Ser Gln His Ser Cys Val Asn Ser 85 90 95

acg gag ctg gat gaa ctc att cag caa ata gtg gca gca ata aat gca 336
Thr Glu Leu Asp Glu Leu Ile Gln Gln Ile Val Ala Ala Ile Asn Ala
100 105 110

		ata Ile 115												-	384
		agt Ser													432
	gga	aac Asn			cgc		-			aaa			_		480
		gcc Ala													528
		gat Asp	-									-			576
	_	acg Thr 195		_			-	-	_		-		-		624
		aca Thr							_	_				_	672
		gcg Ala									_	-	_	_	720
		tat Tyr		 _										_	768
		gca Ala													816
_		tgg Trp 275				-			_			_	-	_	864
		atg Met													912
		gtg Val						_	_				-		960
		gcc Ala							-	_	-				1008
		aag Lys													1056

340 345 350

gaa ctg gct gga aac cac aat cag gag ctg act cct tgt agg agg acc 1104 Glu Leu Ala Gly Asn His Asn Gln Glu Leu Thr Pro Cys Arg Arg Thr 355 360 ctg tca gtg aac cac ctg acc aac gag agg gat gtc ttg cct ccc tta 1152 Leu Ser Val Asn His Leu Thr Asn Glu Arg Asp Val Leu Pro Pro Leu 370 375 ctg aag act gag agt atc tat ctg aat ggt ttg acg cca cac tgt gct 1200 Leu Lys Thr Glu Ser Ile Tyr Leu Asn Gly Leu Thr Pro His Cys Ala 390 395 ggt gaa gag att gct gtg att gag aac atc aaa tag 1236 Gly Glu Glu Ile Ala Val Ile Glu Asn Ile Lys 405 410

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Tyr Val Ala Gly Gly Ser Asp Ile Glu Tyr Leu Asp Phe Tyr Lys Pro 260 265 270 Val Val Trp Phe Trp Ile Leu Val Gly Leu Ala Tyr Phe Ala Ala Val 275 280 Leu Ser Met Ile Gly Asp Trp Leu Arg Val Ile Ser Lys Lys Thr Lys 295 300 Glu Glu Val Gly Glu Phe Arg Ala His Ala Ala Glu Trp Thr Ala Asn Val Thr Ala Glu Phe Lys Glu Thr Arg Arg Arg Leu Ser Val Glu Ile 325 330 Tyr Asp Lys Phe Gln Arg Ala Thr Ser Ile Lys Arg Lys Leu Ser Ala 345 Glu Leu Ala Gly Asn His Asn Gln Glu Leu Thr Pro Cys Arg Arg Thr 360 Leu Ser Val Asn His Leu Thr Asn Glu Arg Asp Val Leu Pro Pro Leu 375 Leu Lys Thr Glu Ser Ile Tyr Leu Asn Gly Leu Thr Pro His Cys Ala 390 395 Gly Glu Glu Ile Ala Val Ile Glu Asn Ile Lys 405

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624

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		_	_	_		cag Gln 70		-				-				720
			_	_	-	acc Thr			-	_		_	_	_		768
			_	-	_	ctc Leu		_				_	-			816
						gga Gly							-			864
						ttc Phe										912
						cca Pro 150										960
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						gga Gly								_		1056
						aag Lys										1104
						ttc Phe		-			-	-				1152
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						gtt Val										1248
						tca Ser						_			_	1296

260 265 270

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														aca Thr		1440
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_		_						_	-	_		_	-	agg Arg		1584
														cct Pro		1632
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			gac Asp		-	-				_	-	tag	ccct	ctct	tg	1729
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Gly Ile Ile Pro Leu Gly Asn Ser Ser Asn Gln Val Ser His Trp Asp
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Ile Tyr Ala Leu Leu Gly Ile Pro Leu Phe Gly Phe Leu Leu Ala Gly
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Val Gly Asp Gln Leu Gly Thr Ile Phe Gly Lys Gly Ile Ala Lys Val
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Glu Asp Thr Phe Ile Lys Trp Asn Val Ser Gln Thr Lys Ile Arg Ile
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Ile Ser Thr Ile Ile Phe Ile Leu Phe Gly Cys Val Leu Phe Val Ala
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Leu Pro Ala Val Ile Phe Lys His Ile Glu Gly Trp Ser Ala Leu Asp
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Ala Ile Tyr Phe Val Val Ile Thr Leu Thr Thr Ile Gly Phe Gly Asp
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Tyr Val Ala Gly Gly Ser Asp Ile Glu Tyr Leu Asp Phe Tyr Lys Pro
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Val Val Trp Phe Trp Ile Leu Val Gly Leu Ala Tyr Phe Ala Ala Val
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Leu Ser Met Ile Gly Asp Trp Leu Arg Val Ile Ser Lys Lys Thr Lys
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Glu Glu Val Gly Glu Phe Arg Ala His Ala Ala Glu Trp Thr Ala Asn
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Val Thr Ala Glu Phe Lys Glu Thr Arg Arg Arg Leu Ser Val Glu Ile
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Tyr Asp Lys Phe Gln Arg Ala Thr Ser Val Lys Arg Lys Leu Ser Ala
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Glu Leu Ala Gly Asn His Asn Gln Glu Leu Thr Pro Cys Arg Arg Thr
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Leu Ser Val Asn His Leu Thr Ser Glu Arg Glu Val Leu Pro Pro Leu
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Arg Ala Arg Tyr Asn Leu Ser Gln Gly Gly Tyr Glu Glu Leu Glu Arg
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65

70

85

Val Ile Gln Lys Gln Thr Phe Ile Ala Gln His Ala Cys Val Asn Ser

90

Val Val Leu Arg Leu Lys Pro His Lys Ala Gly Val Gln Trp Arg Phe Ala Gly Ser Phe Tyr Phe Ala Ile Thr Val Ile Thr Thr Ile Gly Tyr Gly His Ala Ala Pro Ser Thr Asp Gly Gly Lys Val Phe Cys Met Phe Tyr Ala Leu Leu Gly Ile Pro Leu Thr Leu Val Met Phe Gln Ser Leu Gly Glu Arg Ile Asn Thr Leu Val Arg Tyr Leu Leu His Arg Ala Lys Lys Gly Leu Gly Met Arg Arg Ala Asp Val Ser Met Ala Asn Met Val Leu Ile Gly Phe Phe Ser Cys Ile Ser Thr Leu Cys Ile Gly Ala Ala Ala Phe Ser His Tyr Glu His Trp Thr Phe Phe Gln Ala Tyr Tyr Cys Phe Ile Thr Leu Thr Thr Ile Gly Phe Gly Asp Tyr Val Ala Leu Gln Lys Asp Gln Ala Leu Gln Thr Gln Pro Gln Tyr Val Ala Phe Ser Phe Val Tyr Ile Leu Thr Gly Leu Thr Val Ile Gly Ala Phe Leu Asn Leu Val Val Leu Arg Phe Met Thr Met Asn Ala Glu Asp Glu Lys Arg Asp Ala Glu His Arg Ala Leu Leu Thr Arg Asn Gly Gln Ala Gly Gly Gly Gly Gly Gly Ser Ala His Thr Thr Asp Thr Ala Ser Ser Thr Ala Ala Ala Gly Gly Gly Phe Arg Asn Val Tyr Ala Glu Val Leu His Phe Gln Ser Met Cys Ser Cys Leu Trp Tyr Lys Ser Arg Glu Lys Leu Gln Tyr Ser Ile Pro Met Ile Ile Pro Arg Asp Leu Ser Thr Ser Asp Thr Cys Val Glu Gln Ser His Ser Ser Pro Gly Gly Gly Arg Tyr Ser Asp Thr Pro Ser Arg Arg Cys Leu Cys Ser Gly Ala Pro Arg Ser Ala Ile Ser Ser Val Ser Thr Gly Leu His Ser Leu Ser Thr Phe Arg Gly Leu Met Lys Arg Arg Ser Ser Val